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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/954,556

DATE: 10/09/2001
 TIME: 08:54:19

Input Set : A:\RTS-0250_Seq_ASCII.txt
 Output Set: N:\CRF3\10092001\I954556.raw

3 <110> APPLICANT: Brett P. Monia
 4 Susan M. Freier
 5 Scott Cooper
 7 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 2
EXPRESSION
 9 <130> FILE REFERENCE: RTS-0250
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/954,556
 C--> 11 <141> CURRENT FILING DATE: 2001-09-14
 11 <160> NUMBER OF SEQ ID NOS: 108
 14 <210> SEQ ID NO: 1
 15 <211> LENGTH: 20
 16 <212> TYPE: DNA
 17 <213> ORGANISM: Artificial Sequence
 19 <220> FEATURE:
 21 <223> OTHER INFORMATION: Antisense Oligonucleotide
 23 <400> SEQUENCE: 1
 24 tccgtcatcg ctcctcagg
 27 <210> SEQ ID NO: 2
 28 <211> LENGTH: 20
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Artificial Sequence
 32 <220> FEATURE:
 34 <223> OTHER INFORMATION: Antisense Oligonucleotide
 36 <400> SEQUENCE: 2
 37 atgcattctg ccccaagga
 40 <210> SEQ ID NO: 3
 41 <211> LENGTH: 4268
 42 <212> TYPE: DNA
 43 <213> ORGANISM: Homo sapiens
 45 <220> FEATURE:
 47 <220> FEATURE:
 48 <221> NAME/KEY: CDS
 49 <222> LOCATION: (274)...(2739)
 51 <400> SEQUENCE: 3
 52 cccaggacc acttctctgc gtttgaggatt gtcacca accccgggct cgtcgctttc 60
 54 tccatcccgaa cccacgcggg gcgccccggac aacacaggta gcggaggagc gttgccattc 120
 56 aagtgaactgc agcagcagcg gcagcgccctc gtttcttgat cccaccgcag gctgaaggca 180
 58 ttgcgcgttag tccatccccg tagaggaagt gtgcagatgg gattaacgtc cacatggaga 240
 60 tatggaaagag gaccggggat tggtaccgtt acc atg gtc agc tgg ggt cgt ttc 294
 Met Val Ser Trp Gly Arg Phe
 61 1 5
 62
 64 atc tgc ctg gtc gtg gtc acc atg gca acc ttg tcc ctg gcc cgg ccc 342
 65 Ile Cys Leu Val Val Val Thr Met Ala Thr Leu Ser Leu Ala Arg Pro
 66 10 15 20
 68 tcc ttc agt tta gtt gag gat acc aca tta gag cca gaa gag cca cca 390
 69 Ser Phe Ser Leu Val Glu Asp Thr Thr Leu Glu Pro Glu Glu Pro Pro
 70 25 30 35
 72 acc aaa tac caa atc tct caa cca gaa gtg tac gtg gct gcg cca ggg 438

ENTERED

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Input Set : A:\RTS-0250_Seq_ASCII.txt
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73	Thr Lys Tyr Gln Ile Ser Gln Pro Glu Val Tyr Val Ala Ala Pro Gly				
74	40	45	50	55	
76	gag tcg cta gag gtg cgc tgc ctg ttg aaa gat gcc gcc gtg atc agt				486
77	Glu Ser Leu Glu Val Arg Cys Leu Leu Lys Asp Ala Ala Val Ile Ser				
78	60	65	70		
80	tgg act aag gat ggg gtg cac ttg ggg ccc aac aat agg aca gtg ctt				534
81	Trp Thr Lys Asp Gly Val His Leu Gly Pro Asn Asn Arg Thr Val Leu				
82	75	80	85		
84	att ggg gag tac ttg cag ata aag ggc gcc acg cct aga gac tcc ggc				582
85	Ile Gly Glu Tyr Leu Gln Ile Lys Gly Ala Thr Pro Arg Asp Ser Gly				
86	90	95	100		
88	ctc tat gct tgt act gcc agt agg act gta gac agt gaa act tgg tac				630
89	Leu Tyr Ala Cys Thr Ala Ser Arg Thr Val Asp Ser Glu Thr Trp Tyr				
90	105	110	115		
92	tcc atg gtg aat gtc aca gat gcc atc tca tcc gga gat gat gag gat				678
93	Phe Met Val Asn Val Thr Asp Ala Ile Ser Ser Gly Asp Asp Glu Asp				
94	120	125	130	135	
96	gac acc gat ggt gcg gaa gat ttt gtc agt gag aac agt aac aac aag				726
97	Asp Thr Asp Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn Asn Lys				
98	140	145	150		
100	aga gca cca tac tgg acc aac aca gaa aag atg gaa aag cgg ctc cat				774
101	Arg Ala Pro Tyr Trp Thr Asn Thr Glu Lys Met Glu Lys Arg Leu His				
102	155	160	165		
104	gct gtg cct gcg gcc aac act gtc aag ttt cgc tgc cca gcc ggg ggg				822
105	Ala Val Pro Ala Ala Asn Thr Val Lys Phe Arg Cys Pro Ala Gly Gly				
106	170	175	180		
108	aac cca atg cca acc atg cgg tgg ctg aaa aac ggg aag gag ttt aag				870
109	Asn Pro Met Pro Thr Met Arg Trp Leu Lys Asn Gly Lys Glu Phe Lys				
110	185	190	195		
112	cag gag cat cgc att gga ggc tac aag gta cga aac cag cac tgg agc				918
113	Gln Glu His Arg Ile Gly Gly Tyr Lys Val Arg Asn Gln His Trp Ser				
114	200	205	210	215	
116	ctc att atg gaa agt gtg gtc cca tct gac aag gga aat tat acc tgt				966
117	Leu Ile Met Glu Ser Val Val Pro Ser Asp Lys Gly Asn Tyr Thr Cys				
118	220	225	230		
120	gtg gtg gag aat gaa tac ggg tcc atc aat cac acg tac cac ctg gat				1014
121	Val Val Glu Asn Glu Tyr Gly Ser Ile Asn His Thr Tyr His Leu Asp				
122	235	240	245		
124	gtt gtg gag cga tcg cct cac cgg ccc atc ctc caa gcc gga ctg ccg				1062
125	Val Val Glu Arg Ser Pro His Arg Pro Ile Leu Gln Ala Gly Leu Pro				
126	250	255	260		
128	gca aat gcc tcc aca gtg gtc gga gga gac gta gag ttt gtc tgc aag				1110
129	Ala Asn Ala Ser Thr Val Val Gly Gly Asp Val Glu Phe Val Cys Lys				
130	265	270	275		
132	gtt tac agt gat gcc cag ccc cac atc cag tgg atc aag cac gtg gaa				1158
133	Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Ile Lys His Val Glu				
134	280	285	290	295	
136	aag aac ggc agt aaa tac ggg ccc gac ggg ctg ccc tac ctc aag gtt				1206
137	Lys Asn Gly Ser Lys Tyr Gly Pro Asp Gly Leu Pro Tyr Leu Lys Val				

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138	300	305	310	
140	ctc aag gcc gcc ggt gtt aac acc acg gac aaa gag att gag gtt ctc			1254
141	Leu Lys Ala Ala Gly Val Asn Thr Thr Asp Lys Glu Ile Glu Val Leu			
142	315	320	325	
144	tat att cggt aat gta act ttt gag gac gct ggg gaa tat acg tgc ttg			1302
145	Tyr Ile Arg Asn Val Thr Phe Glu Asp Ala Gly Glu Tyr Thr Cys Leu			
146	330	335	340	
148	gct ggt aat tct att ggg ata tcc ttt cac tct gca tgg ttg aca gtt			1350
149	Ala Gly Asn Ser Ile Gly Ile Ser Phe His Ser Ala Trp Leu Thr Val			
150	345	350	355	
152	ctg cca gcg cct gga aga gaa aag gag att aca gct tcc cca gac tac			1398
153	Leu Pro Ala Pro Gly Arg Glu Lys Glu Ile Thr Ala Ser Pro Asp Tyr			
154	360	365	370	375
156	ctg gag ata gcc att tac tgc ata ggg gtc ttc tta atc gcc tgt atg			1446
157	Leu Glu Ile Ala Ile Tyr Cys Ile Gly Val Phe Leu Ile Ala Cys Met			
158	380	385	390	
160	gtg gta aca gtc atc ctg tgc cga atg aag aac acg acc aag aag cca			1494
161	Val Val Thr Val Ile Leu Cys Arg Met Lys Asn Thr Thr Lys Lys Pro			
162	395	400	405	
164	gac ttc agc agc cag ccg gct gtg cac aag ctg acc aaa cgt atc ccc			1542
165	Asp Phe Ser Ser Gln Pro Ala Val His Lys Leu Thr Lys Arg Ile Pro			
166	410	415	420	
168	ctg cgg aga cag gta aca gtt tcg gct gag tcc agc tcc tcc atg aac			1590
169	Leu Arg Arg Gln Val Thr Val Ser Ala Glu Ser Ser Ser Met Asn			
170	425	430	435	
172	tcc aac acc ccg ctg gtg agg ata aca aca cgc ctc tct tca acg gca			1638
173	Ser Asn Thr Pro Leu Val Arg Ile Thr Thr Arg Leu Ser Ser Thr Ala			
174	440	445	450	455
176	gac acc ccc atg ctg gca ggg gtc tcc gag tat gaa ctt cca gag gac			1686
177	Asp Thr Pro Met Leu Ala Gly Val Ser Glu Tyr Glu Leu Pro Glu Asp			
178	460	465	470	
180	cca aaa tgg gag ttt cca aga gat aag ctg aca ctg ggc aag ccc ctg			1734
181	Pro Lys Trp Glu Phe Pro Arg Asp Lys Leu Thr Leu Gly Lys Pro Leu			
182	475	480	485	
184	gga gaa ggt tgc ttt ggg caa gtg gtc atg gcg gaa gca gtg gga att			1782
185	Gly Glu Gly Cys Phe Gly Gln Val Val Met Ala Glu Ala Val Gly Ile			
186	490	495	500	
188	gac aaa gac aag ccc aag gag gcg gtc acc gtg gcc gtg aag atg ttg			1830
189	Asp Lys Asp Lys Pro Lys Glu Ala Val Thr Val Ala Val Lys Met Leu			
190	505	510	515	
192	aaa gat gat gcc aca gag aaa gac ctt tct gat ctg gtg tca gag atg			1878
193	Lys Asp Asp Ala Thr Glu Lys Asp Leu Ser Asp Leu Val Ser Glu Met			
194	520	525	530	535
196	gag atg atg aag atg att ggg aaa cac aag aat atc ata aat ctt ctt			1926
197	Glu Met Met Lys Met Ile Gly Lys His Lys Asn Ile Ile Asn Leu Leu			
198	540	545	550	
200	gga gcc tgc aca cag gat ggg cct ctc tat gtc ata gtt gag tat gcc			1974
201	Gly Ala Cys Thr Gln Asp Gly Pro Leu Tyr Val Ile Val Glu Tyr Ala			
202	555	560	565	

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Input Set : A:\RTS-0250_Seq_ASCII.txt
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204 tct aaa ggc aac ctc cga gaa tac ctc cga gcc cg	agg cca ccc ggg	2022
205 Ser Lys Gly Asn Leu Arg Glu Tyr Leu Arg Ala Arg Arg Pro Pro Gly		
206 570 575 580		
208 atg gag tac tcc tat gac att aac cgt gtt cct gag gag cag atg acc		2070
209 Met Glu Tyr Ser Tyr Asp Ile Asn Arg Val Pro Glu Glu Gln Met Thr		
210 585 590 595		
212 ttc aag gac ttg gtg tca tgc acc tac cag ctg gcc aga ggc atg gag		2118
213 Phe Lys Asp Leu Val Ser Cys Thr Tyr Gln Leu Ala Arg Gly Met Glu		
214 600 605 610 615		
216 tac ttg gct tcc caa aaa tgt att cat cga gat tta gca gcc aga aat		2166
217 Tyr Leu Ala Ser Gln Lys Cys Ile His Arg Asp Leu Ala Ala Arg Asn		
218 620 625 630		
220 gtt ttg gta aca gaa aac aat gtg atg aaa ata gca gac ttt gga ctc		2214
221 Val Leu Val Thr Glu Asn Asn Val Met Lys Ile Ala Asp Phe Gly Leu		
222 635 640 645		
224 gcc aga gat atc aac aat ata gac tat tac aaa aag acc acc aat ggg		2262
225 Ala Arg Asp Ile Asn Asn Ile Asp Tyr Tyr Lys Lys Thr Thr Asn Gly		
226 650 655 660		
228 cgg ctt cca gtc aag tgg atg gct cca gaa gcc ctg ttt gat aga gta		2310
229 Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ala Leu Phe Asp Arg Val		
230 665 670 675		
232 tac act cat cag agt gat gtc tgg tcc ttc ggg gtg tta atg tgg gag		2358
233 Tyr Thr His Gln Ser Asp Val Trp Ser Phe Gly Val Leu Met Trp Glu		
234 680 685 690 695		
236 atc ttc act tta ggg ggc tcg ccc tac cca ggg att ccc gtg gag gaa		2406
237 Ile Phe Thr Leu Gly Gly Ser Pro Tyr Pro Gly Ile Pro Val Glu Glu		
238 700 705 710		
240 ctt ttt aag ctg ctg aag gaa cac aga atg gat aag cca gcc aac		2454
241 Leu Phe Lys Leu Lys Glu Gly His Arg Met Asp Lys Pro Ala Asn		
242 715 720 725		
244 tgc acc aac gaa ctg tac atg atg agg gac tgt tgg cat gca gtg		2502
245 Cys Thr Asn Glu Leu Tyr Met Met Arg Asp Cys Trp His Ala Val		
246 730 735 740		
248 ccc tcc cag aga cca acg ttc aag cag ttg gta gaa gac ttg gat cga		2550
249 Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu Val Glu Asp Leu Asp Arg		
250 745 750 755		
252 att ctc act ctc aca acc aat gag gaa tac ttg gac ctc agc caa cct		2598
253 Ile Leu Thr Leu Thr Asn Glu Glu Tyr Leu Asp Leu Ser Gln Pro		
254 760 765 770 775		
256 ctc gaa cag tat tca cct agt tac cct gac aca aga agt tct tgt tct		2646
257 Leu Glu Gln Tyr Ser Pro Ser Tyr Pro Asp Thr Arg Ser Ser Cys Ser		
258 780 785 790		
260 tca gga gat gat tct gtt ttt tct cca gac ccc atg cct tac gaa cca		2694
261 Ser Gly Asp Asp Ser Val Phe Ser Pro Asp Pro Met Pro Tyr Glu Pro		
262 795 800 805		
264 tgc ctt cct cag tat cca cac ata aac ggc agt gtt aaa aca tga		2739
265 Cys Leu Pro Gln Tyr Pro His Ile Asn Gly Ser Val Lys Thr		
266 810 815 820		
268 atgactgtgt ctgcctgtcc ccaaacagga cagcactggg aaccttagcta cactgagcag		2799

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Input Set : A:\RTS-0250_Seq_ASCII.txt
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270	ggagaccatg cctccagag cttgttgtct ccacttgtat atatggatca gaggagtaaa	2859
272	taattggaaa agtaatcagc atatgtgtaa agatttatac agttaaaaac ttgtaatctt	2919
274	ccccaggagg agaagaagg ttcgttgagca gtggactgcc acaagccacc atgtacccc	2979
276	tctcacctgc cgtcggttct ggctgtggac cagtaggact caaggtggac gtgcgttctg	3039
278	ccttcattgt taattttgtataa attttggag aagattttatg tcagcacaca cttacagagc	3099
280	acaaatgcag tatatagggtt ctggatgtat gtaaatatat tcaaatttatg tataaatata	3159
282	tattatataat ttacaaggag ttatTTTt tattttttt aaatggatgt cccaatgcac	3219
284	ctagaaaatt ggtctctttt ttttaataag ctatttgcta aatgctttc ttacacataa	3279
286	tttcttaatt ttcaccgagc agaggtggaa aaatactttt gctttcaggg aaaatggat	3339
288	aacgttaatt tattaataaa ttggtaatataa acaaaaacaat taatcattta tagtttttt	3399
290	tgttaattaa gtggattttc tatgcagggca gcacagcaga ctgttaatc tattgcttgg	3459
292	acttaacttag ttatcagatc ctttggaaaag agaatattta caatataatga ctaatttggg	3519
294	aaaaatgaag ttttgattta tttgtgttta aatgctgtg tcagacgatt gttcttagac	3579
296	ctcctaaatg ccccatatta aaagaactca ttcataggaa ggtgtttcat tttgggtgtc	3639
298	aaccctgtca ttacgtcaac gcaacgtcta actggacttc ccaagataaa tggaccagc	3699
300	gtcctttaa aagatgcctt aatccatttc ttgaggacag accttagttt aatgatagc	3759
302	agaatgtgtct tctctctggc agctggccctt ctgcttctga gttgcacatt aatcagatta	3819
304	gcctgattct cttcaagtggaa ttttggataat ggcttccaga ctctttcggt tggagacgcc	3879
306	tgttaggatc ttcaagtccc atcatagaaa attggaaacac agagttttc tgctgatagt	3939
308	tttggggata cgtccatctt ttaaggat tgcttcatc taattctggc aggacctcac	3999
310	caaaagatcc agcctcatac ctacatcaga caaaatatacg ccgttgcgttcc ttctgtacta	4059
312	aagtattgtt ttttggatggaaacaccca ctcacttgc aatagccgtg caagatgaat	4119
314	gcagattaca ctgatctt gtttggatggaaacaccca aatgatgttca cagatattaa tgttaacaag acaaaaataaa	4179
316	atttttatac tgacaataaaa aatgatgttca cagatattaa tgttaacaag acaaaaataaa	4239
318	tgtcacgcaaa cttaaaaaaaaaaaaaaaa	4268
321	<210> SEQ ID NO: 4	
322	<211> LENGTH: 22	
323	<212> TYPE: DNA	
324	<213> ORGANISM: Artificial Sequence	
326	<220> FEATURE:	
328	<223> OTHER INFORMATION: PCR Primer	
330	<400> SEQUENCE: 4	
331	aaggaccact cttctcggtt tg	22
334	<210> SEQ ID NO: 5	
335	<211> LENGTH: 19	
336	<212> TYPE: DNA	
337	<213> ORGANISM: Artificial Sequence	
339	<220> FEATURE:	
341	<223> OTHER INFORMATION: PCR Primer	
343	<400> SEQUENCE: 5	
344	tgggtcgaaa tggagaaaag	19
347	<210> SEQ ID NO: 6	
348	<211> LENGTH: 20	
349	<212> TYPE: DNA	
350	<213> ORGANISM: Artificial Sequence	
352	<220> FEATURE:	
354	<223> OTHER INFORMATION: PCR Probe	
356	<400> SEQUENCE: 6	
357	cccacaaaccc cgggctcgtc	20

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\RTS-0250_Seq_ASCII.txt
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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1191 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1192 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1193 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1603 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1604 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1605 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:5150 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:5413 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29